CLAIMS

What is claimed is:

1. A method for predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy comprising determining whether the HBV carried by the host (i) bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region (originally codon 438); or a (ii) a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV.

2. A method for predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy comprising determining whether the HBV carried by the host bears one or more of the following mutations: (i) Q213S (glutamine to serine at aa213) (originally codon 604) in the HBV polymerase region; (ii) G1739T, A1752C/T, T1909C, T1960G, or T1961A/G specific point mutation in the DNA precore/ core promoter or open reading frame (ORF) region; or (iii) a pair of nucleotide changes A1738C and G1739T;, A1750G and A1752G; T1909G and A1911T; or T1961A and C1962A representing specific double point mutations in the DNA precore/core promoter or open reading frame (ORF) region.

3. The method of claim 1 that determines whether the HBV carried by the host bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region.

4. The method of claim 1 that determines whether the HBV carried by the host bears a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV.

5. The method of claim 2 that determines whether the HBV carried by the host bears mutation Q213S (glutamine to serine at aa213) in the HBV polymerase region.

6. The method of claim 2 that determines whether the HBV carried by the host bears mutation G1739T in the DNA precore/ core promoter or open reading frame (ORF) region.

7. The method of claim 2 that determines whether the HBV carried by the host bears mutation A1752C/T in the DNA precore/ core promoter or open reading frame (ORF) region.

8. The method of claim 2 that determines whether the HBV carried by the host bears mutation T1909C in the DNA precore/ core promoter or open reading frame (ORF) region.

9. The method of claim 2 that determines whether the HBV carried by the host bears mutation T1960G in the DNA precore/ core promoter or open reading frame (ORF) region.

10. The method of claim 2 that determines whether the HBV carried by the host bears mutation T1961A/G in the DNA precore/ core promoter or open reading frame (ORF) region.

11. The method of claim 2 wherein the HBV bears a pair of nucleotide changes A1738C and G1739T representing specific double point mutations in the DNA precore/core promoter or open reading frame (ORF) region.

12. The method of claim 2 wherein the HBV bears a pair of nucleotide changes A1750G and A1752G representing specific double point mutations in the DNA precore/core promoter or open reading frame (ORF) region.

13. The method of claim 2 wherein the HBV bears a pair of nucleotide changes T1909G and A1911T representing specific double point mutations in the DNA precore/core promoter or open reading frame (ORF) region.

14. The method of claim 2 wherein the HBV bears a pari of nucleotide changes T1961A and C1962A representing specific double point mutations in the DNA precore/core promoter or open reading frame (ORF) region.

15. A method for determining the long term response of an HBV carrier to 3TC therapy, comprising determining whether a biological sample from the carrier contains an HBV protein, peptide, or peptide fragment that is encoded by a nucleic acid described in claim 1.

16. A method for determining the long term response of an HBV carrier to 3TC therapy, comprising determining whether a biological sample from the carrier contains an HBV protein, peptide, or peptide fragment that is encoded by a nucleic acid described in claim 2.

17. The method of claim 16, wherein the protein, peptide, or peptide fragment viral markers is detected by a method selected from the group consisting of western blot assay, two dimensional gel electrophoresis (2D-PAGE), enzyme linked immunosorbent assays (ELISA), enhanced chemiluminescence (ECL), immunohistochemistry, ELI-Spot assays, peptide sequencing, and antibody based protein array technology.

18. The method of claim 1, wherein the carrier is HBeAg negative.

19. The method of claim 2, wherein the carrier is HBeAg negative.

20. The method of claim 15, wherein the carrier is HBeAg negative.

21. The method of claim 16, wherein the carrier is HBeAg negative.

22. The method of claim 1 or 2, wherein the HBV nucleic acid sequence is determined by contact with a oligonucleotide probe having a sequence complementary to a section of the gene that includes the viral marker.

23. The method of claim 22, wherein probe is labeled probe using a detectable agent.

24. The method of claim 23, wherein the probe is labeled with a material selected from the grout consisting of a radioisotope, biotin, fluorescent dye, electron-dense reagent, enzyme, hapten or protein for which antibodies are available.

25. The method of claim 23, wherein the detectable label is assayed by spectroscopic, photochemical, biochemical, immunochemical, radioisotopic, or chemical means.

26. The method of claim 23, wherein the probe is detected by an oligomer restriction technique, a dot blot assay, a reverse dot blot assay, a line probe assay, or a 5' nuclease assay.

27. The method of claim 23, wherein the probe is detected using DNA array technology.

28. The method of claim 27, wherein the probe is detected using a macroarray.

29. The method of claim 27, wherein the probe is detected using a microarray.

30. The method of claim 27, wherein the probe is detected using DNA microchip technology.

31. A nucleic acid sequence selected from the group consisting of Seq. Id Nos. 1-351 or an oligonucleotide which hybridizes under stringent conditions to a sequence selected from the group consisting of Seq. Id Nos. 1-351.

32. A nucleic acid sequence of 14 to 28 nucleotides illustrated in the embodiments of Tables 1-13 of Seq. Id Nos. 1-351 or an oligonucleotide which hybridizes under stringent conditions to a nucleic acid sequence of 14 to 28 nucleotides illustrated in the embodiments of Tables 1-13 of Seq. Id Nos. 1-351.

33. A kit for predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy comprising reagents to determine whether the HBV carried by the host bears a nucleic acid that encodes for a leucine at amino acid position (aa) 91 in the DNA polymerase region (originally codon 438).

34. A kit for predicting the long term response of a host of hepatitis B virus (HBV) to 3TC therapy comprising reagents to determine whether the HBV carried by the host bears a cysteine at aa256 (originally codon 604) in the DNA polymerase region of HBV.

35. A kit for predicting the long term response of an HBV carrier to 3TC therapy, comprising reagents that can determine whether a biological sample from the carrier contains an HBV protein, peptide, or peptide fragment that is encoded by a nucleic acid described in claim 1.

36. A kit for predicting the long term response of an HBV carrier to 3TC therapy, comprising reagents that determining whether a biological sample from the carrier contains an HBV protein, peptide, or peptide fragment that is encoded by a nucleic acid described in claim 2.